Original Article

Prevalence of *bla*$_{CTX-M}$ Gene in Multi-Resistant *Escherichia coli* Isolated from Urinary Tract Infections, Tehran, Iran

Mehdi Goudarzi[1,2], Fattaneh Sabzehali[2], Zahra Tayebi[3], Mehdi Azad[4], Shahram Boromandi[5], Ali Hashemi[2], Sima Sadat Seyedjavadi[6*]

[1] Infectious Diseases and Tropical Medicine Research Center, Shahid Beheshti University of Medical Science, Tehran, Iran
[2] Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Science, Tehran, Iran
[3] Department of Microbiology, Tehran Medical Branch, Islamic Azad University, Tehran, Iran
[4] Faculty of paramedical sciences, Qazvin University of Medical Sciences, Qazvin, Iran
[5] Department of Microbiology, Pars hospital laboratory
[6] Department of Pharmaceutical Biotechnology, Pasteur institute, Tehran, Iran

Abstract

Background: The emergence and increase in the incidence of Extended-spectrum beta lactamase (ESBL) producing *Escherichia coli* (*E. coli*) has become an emerging challenge especially in hospitalized patients with urinary tract infection (UTI). The aim of the present study was to survey the frequency of *bla* CTX-M genotype in ESBL producing *E. coli* isolated from hospitalized patients with urinary tract infection and determination of their antibiotic resistance pattern.

Materials and Methods: A total of 135 *E. coli* isolates were collected and isolated from patients with UTI. The isolates were subjected to confirmatory phenotype tests for the presence of ESBL. 75 *E. coli* isolates were confirmed as ESBL-positive by double disc synergy test. In vitro susceptibility of ESBL isolates to 15 antimicrobial agents amoxicillin, penicillin, ceftazidime, cefotaxime, cefoxitin, ceftriaxone, cefixime, cephalexin, co-trimoxazole, gentamicin, nalidixic acid, ciprofloxacin, nitrofurantoin, amikacin, and imipenem was performed by Kirby-Bauer's Disk diffusion method according to Clinical and Laboratory Standards Institute (CLSI, 2012) guideline. PCR method was used to identify *bla* CTX-M gene in 75 ESBL positive strains.

Results: PCR and sequence analysis showed that 75 (55.5%) isolates produced *bla* CTX-M genes. In vitro susceptibility of ESBL producing *E. coli* showed that all of them were resistant to amoxicillin and penicillin. The rates of resistance to the majority of tested antibiotics varied among 61% to 100 %, with the exception of amikacin (14.7%) and imipenem (2.7%). Our results showed that the frequency of *bla* CTX-M was strikingly high (93.3%) in patients with UTI.

Conclusion: These data confirmed that the frequency of *bla* CTX-M genes was high among *E. coli* isolated from patients with UTI. The trend of multidrug-resistant profile has been associated with *bla* CTX-M gene is alarming. Therefore, it is very important to establish a routine screening of ESBL in clinical isolates to prevent dissemination of resistant isolates in health care settings.

Keywords: ESBL, Beta lactamase, *Escherichia coli*, antimicrobial resistance

***Corresponding Author:** Sima Sadat Seyedjavadi, Department of Pharmaceutical Biotechnology, Pasteur institute, Tehran, Iran. Email: Sima_seyedjavadi@yahoo.com

Please cite this article as: Goudarzi M, Sabzehali F, Tayebi Z, Azad M, Boromani SH, Hashemi A, Seyedjavadi SS. Prevalence of *bla*$_{CTX-M}$ Gene in Multi-Resistant *Escherichia coli* Isolated from Urinary Tract Infections, Tehran, Iran. Novel Biomed. 2014;2(4):107-13.